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U.S. APPLICATION NUMBER NO.	FIRST NAMED APPLICANT	ATTY. DOCKET NO.
10/591,752	Akiho Yokota	2006_1303A

513
 WENDEROTH, LIND & PONACK, L.L.P.
 2033 K STREET N. W.
 SUITE 800
 WASHINGTON, DC 20006-1021

RECEIVED
 MAY 14 2007

WENDEROTH, LIND & PONACK

INTERNATIONAL APPLICATION NO.

PCT/JP05/04037

I.A. FILING DATE

03/02/2005

PRIORITY DATE

03/03/2004

CONFIRMATION NO. 3250

371 FORMALITIES LETTER



OC000000023821838

Date Mailed: 05/11/2007

NOTIFICATION TO COMPLY WITH REQUIREMENTS FOR PATENT APPLICATIONS CONTAINING NUCLEOTIDE AND/OR AMINO ACID SEQUENCE DISCLOSURES

Applicant is given **TWO MONTHS FROM THE DATE OF THIS NOTICE** within which to file the items indicated below to avoid abandonment. Extensions of time may be obtained under the provisions of 37 CFR 1.136(a).

- This application clearly fails to comply with the requirements of 37 CFR. 1.821-1.825. Applicant's attention is directed to the final rulemaking notice published at 55 FR 18230 (May 1, 1990), and 1114 OG 29 (May 15, 1990). If the effective filing date is on or after July 1, 1998, see the final rulemaking notice published at 63 FR 29620 (June 1, 1998) and 1211 OG 82 (June 23, 1998). If the effective filing date is on or after September 8, 2000, see the final rulemaking notice published in the Federal Register at 65 FR 54604 (September 8, 2000) and 1238 OG 145 (September 19, 2000). Applicant must provide an initial computer readable form (CRF) copy of the "Sequence Listing", an initial paper or compact disc copy of the "Sequence Listing", as well as an amendment specifically directing its entry into the application. Applicant must also provide a statement that the content of the sequence listing information recorded in computer readable form is identical to the written (on paper or compact disc) sequence listing and, where applicable, includes no new matter, as required by 37 CFR 1.821(e), 1.821(f), 1.821(g), 1.825(b), or 1.825(d). If applicant desires the sequence listing in the instant application to be identical with that of another application on file in the U.S. Patent and Trademark Office, such request in accordance with 37 CFR 1.821(e) may be submitted in lieu of a new CRF.
- A copy of the "Sequence Listing" in computer readable form has been submitted. However, the content of the computer readable form does not comply with the requirements of 37 CFR 1.822 and/or 1.823, as indicated on the attached copy of the marked-up "Raw Sequence Listing." Applicant must provide a substitute computer readable form (CRF) copy of the "Sequence Listing" and a statement that the content of the sequence listing information recorded in computer readable form is identical to the written (on paper or compact disc) sequence listing and, where applicable, includes no new matter, as required by 37 CFR 1.821(e), 1.821(f), 1.821(g), 1.825(b), or 1.825(d).

Applicant is cautioned that correction of the above items may cause the specification and drawings page count to exceed 100 pages. If the specification and drawings exceed 100 pages, applicant will need to submit the required application size fee.

For questions regarding compliance to 37 CFR 1.821-1.825 requirements, please contact:

- For Rules Interpretation, call (571) 272-0951
- For Patent Software Program Help, call Patent EBC at 1-866-217-9197 or directly at 703-305-3028 /

703-308-6845 between the hours of 6 a.m. and 12 midnight, Monday through Friday, EST.

- **Send e-mail correspondence for Patent Software Program Help @ ebc@uspto.gov**

Applicant is reminded that any communications to the United States Patent and Trademark Office must be mailed to the address given in the heading and include the U.S. application no. shown above (37 CFR 1.5)

Registered users of EFS-Web may alternatively submit their reply to this notice via EFS-Web.

<https://sportal.uspto.gov/authenticate/AuthenticateUserLocalEPF.html>

For more information about EFS-Web please call the USPTO Electronic Business Center at 1-866-217-9197 or visit our website at <http://www.uspto.gov/ebc>.

If you are not using EFS-Web to submit your reply, you must include a copy of this notice.

VONDA M WALLACE

Telephone: (703) 308-9140 EXT 225

PART 1 - ATTORNEY/APPLICANT COPY

U.S. APPLICATION NUMBER NO.	INTERNATIONAL APPLICATION NO.	ATTY. DOCKET NO.
10/591,752	PCT/JP05/04037	2006_1303A

FORM PCT/DO/EO/922 (371 Formalities Notice)

STIC Biotechnology Systems Branch

RAW SEQUENCE LISTING **ERROR REPORT**

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 10/591,752
Source: TEWP
Date Processed by STIC: 09/21/2006

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,**
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY**

FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 4.4.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

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Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

- 1. EFS-Bio (<<http://www.uspto.gov/ebc/efs/downloads/documents.htm>> , EFS Submission User Manual - ePAVE)**
- 2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450**
- 3. Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 01/14/05):
U.S. Patent and Trademark Office, Mail Stop Sequence, Customer Window, Randolph Building, 401 Dulany Street, Alexandria, VA 22314**

Revised 01/10/06



IFWP

RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/591,752

DATE: 09/21/2006

TIME: 11:36:46

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5 Technology for the Earth and Kinki University

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W--> 7 <130> FILE REFERENCE: C01F1576

C--> 8 <140> CURRENT APPLICATION NUMBER: US/10/591,752

C--> 8 <141> CURRENT FILING DATE: 2006-09-01

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Does Not Comply
Corrected Diskette Needed
CP8-1, 2, 3, 5, 6, 7, 8

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21 35 40 45

22 Leu Ala Cys Lys Gln Ile Ala Ser Leu Val Gln Arg Ala Gly Ile Ser

23 50 55 60

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25 65 70 75 80

26 Lys Lys Leu Asp Val Val Ser Asn Glu Val Phe Ser Ser Cys Leu Arg

27 85 90 95

28 Ser Ser Gly Arg Thr Gly Ile Ile Ala Ser Glu Glu Glu Asp Val Pro

29 100 105 110

30 Val Ala Val Glu Glu Ser Tyr Ser Gly Asn Tyr Ile Val Val Phe Asp

31 115 120 125

32 Pro Leu Asp Gly Ser Ser Asn Ile Asp Ala Ala Val Ser Thr Gly Ser

33 130 135 140

34 Ile Phe Gly Ile Tyr Ser Pro Asn Asp Glu Cys Ile Val Asp Ser Asp

35 145 150 155 160

36 His Asp Asp Glu Ser Gln Leu Ser Ala Glu Glu Gln Arg Cys Val Val

37 165 170 175

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RAW SEQUENCE LISTING

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 48 Lys Glu Pro Gly Glu Ser Gln Lys Pro Tyr Ser Ser Arg Tyr Ile Gly
 49 260 265 270
 50 Ser Leu Val Gly Asp Phe His Arg Thr Leu Leu Tyr Gly Gly Ile Tyr
 51 275 280 285
 52 Gly Tyr Pro Arg Asp Ala Lys Ser Lys Asn Gly Lys Leu Arg Leu Leu
 53 290 295 300
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 55 305 310 315 320
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Mandatory
numeric
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RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/591,752

DATE: 09/21/2006

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404 accatatgcg gtgtgaaata ccgcacagat gcgtaaggag aaaataccgc atcaggcgcg 240

405 attcgccatt caggctgcgc aactgtttggg aagggcgacg ggtgcggggc tcttcgctat 300

406 tacgccagct ggcgaaaggg ggatgtgctg caaggcgatt aagttgggta acgccagggt 360

407 tttcccagtc acgacgttgt aaaacgacgg ccagtgaatt catgagttgt agggagggat 420

408 ttatgtcacc acaaacagag actaaagcaa gtgttggtt caaagctggt gttaaagagt 480

409 acaaattgac ttattatact cctgagtacc aaaccaagga tactgatata ttggcagcat 540

410 tccgagtaac tcctcaacct ggagttccac ctgaagaagc agggggccgcg gtagctgccg 600

411 aatcttctac tggatcatgg acaactgtat ggaccgatgg acttaccagc cttgatcgtt 660

412 acaaagggcg atgctaccgc atcgagcgtg ttgttgagaa aaaagatcaa tatattgctt 720

413 atgtagctta cccttttagac ctttttgaag aaggttctgt taccaacatg tttacttcca 780

414 ttgtaggtaa cgtatttggg ttcaaagccc tgccgcgtct acgtctggaa gatctgcgaa 840

415 tccctcctgc ttatgttaaa actttccaag gtccgcctca tgggatccaa gttgaaagag 900

416 ataaattgaa caagtatggt cgtcccctgt tgggatgtac tattaaacct aaattggggt 960

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417	tatctgctaa	aaactacggt	agagccggtt	atgaatgtct	tcgcggtgga	cttgatttta	1020
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419	tttgtgccga	agcactttat	aaagcacagg	ctgaaacagg	tgaaatcaaa	gggcattact	1140
420	tgaatgctac	tgcaggtaca	tgcgaagaaa	tgatcaaaag	agctgtattt	gctagagaat	1200
421	tgggcgttcc	gatcgtaatg	catgactact	taacgggggg	attcaccgca	aatactagct	1260
422	tggctcatta	ttgccgagat	aatggtctac	ttcttcacat	ccaccgtgca	atgcatgcgg	1320
423	ttattgatag	acagaagaat	catggtatcc	acttccgggt	attagcaaaa	gcgttacgta	1380
424	tgtctggtgg	agatcatatt	cactctggta	ccgtagtagg	taaacttgaa	ggtgaaagag	1440
425	acataacttt	gggctttggt	gatttactgc	gtgatgattt	tgttgaaaca	gatcgaagtc	1500
426	gcggtattta	tttcaactca	gattgggtct	ctttaccagg	tgttctaccc	gtggcttcag	1560
427	gaggtattca	cgtttggeat	atgcctgctc	tgaccgagat	ctttggggat	gattccgtac	1620
428	tacagttcgg	tggaggaact	ttaggacatc	cttggggtaa	tgcgccagggt	gccgtagcta	1680
429	atcgagtagc	tctagaagca	tgtgtaaaag	ctcgtaatga	aggacgtgat	cttgctcagg	1740
430	aaggtaatga	aattattcgc	gaggcttgca	aatggagccc	ggaactagct	gctgcttggt	1800
431	aagtatggaa	agagatcgta	tttaattttg	cagcagtgga	cgttttggat	aagtaaaaac	1860
432	agtagacatt	agcagataaa	ttagcaggaa	ataaagaagg	ataaggagaa	agaactcaag	1920
433	taattatcct	tgcgttctct	aattgaattg	caattaaact	cggcccaatc	ttttactaaa	1980
434	aggattgagc	cgaatacaac	aaagattcta	ttgcataatat	tttgactaag	tatatactta	2040
435	cctagatata	caagatttga	aatacaaaaat	ctagaaaact	aatcaaaaat	ctaagactca	2100
436	aatcttttcta	ttgttgtctt	ggatcgcggc	cgcgctagcg	tcgacgatcc	ttaggattgg	2160
437	tatattcttt	tctatcctgt	agtttgtagt	ttccctgaat	caagccaagt	atcacacctc	2220
438	tttctacceca	tcctgtatat	tgtccccttt	gttccgtgtt	gaaatagaac	cttaatttat	2280
439	tacttatttt	tttattaaat	tttagatttg	ttagtatta	gatattagta	ttagacgaga	2340
440	ttttacgaaa	caattatttt	tttatttctt	tataggagag	gacaaatctc	ttttttcgat	2400
441	gcgaatttga	cacgacatag	gagaagccgc	cctttattaa	aaattatatt	attttaaata	2460
442	atataaaggg	ggttccaaca	tattaatata	tagtgaagtg	ttccccaga	ttcagaactt	2520
443	tttttcaata	ctcacaatcc	ttattagtta	ataatcctag	tgattggatt	tctatgctta	2580
444	gtctgatagg	aaataagata	ttcaaataaa	taattttata	gcgaatgact	attcatctat	2640
445	tgtattttca	tgcaaatagg	gggcaagaaa	actctatgga	aagatggtgg	tttaattcga	2700
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447	gtcctattga	aaataccaat	gaagatccaa	atcgaaaagt	gaaaaacatt	catagttgga	2820
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449	ggaatttcat	ctctgatgac	acttttttag	ttagttagat	gaatggagac	agttattcca	2940
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451	aactagaaag	ttctttttat	agttatcgaa	actcgaatta	tcggaataat	ggatttaggg	3060
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453	ttaatagttg	cattgatagt	tatcttcagt	ctcaaactctg	tatagatact	tccattataa	3180
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455	gaaatagtag	tgaaaacgag	ggttccagta	gacgaactcg	cacgaagggc	agtgatttaa	3300
456	ctataagaga	aagttctaata	gatctcgacc	tgcaggcatg	caagcttggc	gtaatcatgg	3360
457	tcatagctgt	ttcctgtgtg	aaattgttat	ccgctcacia	ttccacacia	catacgagcc	3420
458	ggaagcataa	agtgtaaagc	ctgggggtgcc	taatgagtga	gctaactcac	attaattgcg	3480
B--> 459	ttgcgctcac	tgccegtttt	ccagtcggga	aacctgtcgt	gccagctgca	ttaatgaatc	3540
460	ggccaacgcg	cggggagagg	cggtttgctg	attgggcgct	cttccgcttc	ctcgctcact	3600
461	gactcgctgc	gctcggtcgt	tgggtgcgg	cgagcggtat	cagctcactc	aaaggcggtg	3660
462	atacggttat	ccacagaatc	aggggataac	gcaggaaaga	acatgtgagc	aaaaggccag	3720
463	caaaaggcca	ggaaccgtaa	aaaggccgcg	ttgctggcgt	ttttccatag	gctccgcccc	3780
464	cctgacgagc	atcacaaaaa	tgcagctca	agtcagaggt	ggcgaaaccc	gacaggacta	3840
465	taaagatacc	aggcgtttcc	ccctggaagc	tccctcgtgc	gctctcctgt	tccgaccctg	3900

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466 ccgcttaccg gatacctgtc cgcctttctc ccttcgggaa gcgtggcgct ttctcaatgc 3960
467 tcacgctgta ggtatctcag ttcggtgtag gtcgttcgct ccaagctggg ctgtgtgcac 4020
468 gaaccccccg ttcagcccga ccgctgcgcc ttatccggta actatcgtct tgagtccaac 4080
469 ccggttaagac acgacttate gccactggca gcagccactg gtaacaggat tagcagagcg 4140
470 aggtatgtag gcggtgctac agagttcttg aagtgggtggc ctaactacgg ctacactaga 4200
471 aggacagtat ttggtatctg cgtctctgctg aagccagtta ccttcggaaa aagagttggt 4260
472 agctcttgat ccggcaaaaca aaccaccgct ggtagcgggtg gtttttttgt ttgcaagcag 4320
473 cagattacgc gcagaaaaaa aggatctcaa gaagatcctt tgatcttttc tacgggggtct 4380
474 gacgctcagt ggaacgaaaa ctcacgttaa gggatttttg tcatgagatt atcaaaaagg 4440
475 atcttcacct agatcctttt aaattaaaaa tgaagtttta aatcaatcta aagtatatat 4500
476 gagtaaactt ggtctgacag ttaccaatgc ttaatcagtg aggcacctat ctcagcgatc 4560
477 tgtctatttc gttcatecat agttgcctga ctcccgcgct tgtagataac tacgatacgg 4620
478 gagggcttac catctggccc cagtgtctga atgataccgc gagaccacg ctcaccggct 4680
479 ccagatttat cagcaataaa ccagccagcc ggaagggccg agcgcagaag tggctctgca 4740
480 actttatccg cctccatcca gtctattaat tgttgccggg aagctagagt aagtagttcg 4800
481 ccagttaata gtttgcgcaa cgttggtgcc attgctacag gcacgtggtg gtcacgctcg 4860
482 tcgtttggtg tggcttcatt cagctccggt tcccaacgat caaggcgagt tacatgatcc 4920
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484 ttggcccgag gtttatcact catggttatg gcagcactgc ataattctct tactgtcttg 5040
485 ccatccgtaa gatgcttttc tgtgactggt gagtactcaa ccaagtcatt ctgagaatag 5100
486 tgtatgcggc gaccgagttg ctcttgcccg gcgtcaatac gggataatac cgcgccacat 5160
487 agcagaactt taaaagtgt catcattgga aaacgttctt cggggcgaaa actctcaagg 5220
488 atcttaccgc tgttgagatc cagttcgatg taaccactc gtgcaccaa ctgatcttca 5280
489 gcacctttta ctttcaccag cgtttctggg tgagcaaaaa caggaaggca aaatgccgca 5340
490 aaaaagggaa taagggcgac acggaaatgt tgaatactca tactcttctt ttttcaatat 5400
491 tattgaagca tttatcaggg ttattgtctc atgagcggat acatatttga atgtatttag 5460
492 aaaaataaac aaataggggt tccgcgcaca tttccccgaa aagtgccacc tgacgtctaa 5520
493 gaaaccatta ttatcatgac attaacctat aaaaataggc gtatcacgag gccctttcgt 5580
494 c 5581

```

495 <210> SEQ ID NO: 15

496 <211> LENGTH: 1434

497 <212> TYPE: DNA

498 <213> ORGANISM: Nicotiana tabacum

499 <223> OTHER INFORMATION: rbcl

500 <400> SEQUENCE: 15

```

501 atgtcaccac aaacagagac taaagcaagt gttggattca aagctgggtg taaagagtac 60
502 aaattgactt attatactcc tgagtaccaa accaaggat actgatataa ggcagcattc 120
503 cgagtaactc ctcaacctgg agttccacct gaagaagcag gggccgcggt agctgccgaa 180
504 tcttctactg gtacatggac aactgtatgg accgatggac ttaccagcct tgatcgttac 240
505 aaagggcgat gctaccgcat cgagcgtggt gttggagaaa aagatcaata tattgcttat 300
506 gtagcttacc ctttagacct ttttgaagaa ggttctgtta ccaacatgtt tacttccatt 360
507 gtaggtaacg tatttgggtt caaagccctg cgcgctctac gtctggaaga tctgcgaatc 420
508 cctcctgctt atgttaaaac tttccaaggt ccgcctcatg ggatccaagt tgaaagagat 480
509 aaattgaaca agtatggteg tcccctgttg ggatgtacta ttaaacctaa attggggtta 540
510 tctgctaaaa actacggtag agccgtttat gaatgtcttc gcggtggact tgattttact 600
511 aaagatgatg agaacgtgaa ctcacaacca tttatgcgtt ggagagatcg tttcttattt 660
512 tgtgccgaag cactttataa agcacaggct gaaacagggt aaatcaaagg gcattacttg 720
513 aatgctactg caggtacatg cgaagaaatg atcaaaagag ctgtatttgc tagagaattg 780
514 ggcgttccga tcgtaatgca tgactactta acggggggat tcaccgcaaa tactagcttg 840

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515 gctcattatt gccgagataa tgggtctactt cttcacatcc accgtgcaat gcatgcggtt      900
516 attgatagac agaagaatca tggatatccac ttccgggtat tagcaaaagc gttacgtatg      960
517 tctgggtggag atcatattca ctctgggtacc gtagtaggta aacttgaagg tgaaagagac     1020
518 ataactttgg gctttgttga tttactgcgt gatgattttg ttgaacaaga tcgaagtcgc      1080
519 ggtattttatt tcaactcaaga ttgggtctct ttaccagggt ttctaccggt ggcttcagga     1140
520 ggtattcacg tttggcatat gcctgctctg accgagatct ttgggggatga ttccgtacta     1200
521 cagttcgggtg gaggaacttt aggacatcct tggggtaatg cgccagggtgc cgtagctaata     1260
522 cgagtagctc tagaagcatg tgtaaaagct cgtaatgaag gacgtgatct tgctcaggaa     1320
523 ggtaaatgaaa ttattcgcga ggcttgcaaa tggagcccgg aactagctgc tgcttgtgaa     1380
524 gtatggaaaag agatcgtatt taattttgca gcagtggacg ttttggataa gtaa           1434

```

525 <210> SEQ ID NO: 16

526 <211> LENGTH: 705

527 <212> TYPE: DNA

528 <213> ORGANISM: Nicotiana tabacum

529 <223> OTHER INFORMATION: accD

530 <400> SEQUENCE: 16

```

531 aatgactatt catctattgt attttcatgc aaataggggg caagaaaact ctatggaaag      60
532 atgggtggttt aattcgatgt tgtttaagaa ggagttcgaa cgcagggtgt ggctaaataa     120
533 atcaatgggc agtcttggtc ctattgaaaa taacaatgaa gatccaaatc gaaaagtga      180
534 aacattcat agttggagga atcgtgacaa ttctagttgc agtaatgttg attatttatt     240
535 cggcggttaaa gacattcgga atttcatctc tgatgacact tttttagtta gtgataggaa     300
536 tggagacagt tattccatct attttgatat tgaaaatcat atttttgaga ttgacaacga     360
537 tcattctttt ctgagtgaac tagaaagttc tttttatagt tatcgaaact cgaattatcg     420
538 gaataatgga tttaggggag aagatcccta ctataattct tacatgtatg atactcaata     480
539 tagttggaat aatcacatta atagttgcat tgatagttat cttcagttct aaatctgtat     540
540 agatacttcc attataagtg gtagtgagaa ttacgggtgac agttacattt ataggggcgt      600
541 ttgtgggtggt gaaagtcgaa atagtagtga aaacgagggt tccagtagac gaactcgcac     660
542 gaagggcagt gatttaacta taagagaaaag ttctaataat ctcga           705

```

543 <210> SEQ ID NO: 17

544 <211> LENGTH: 21

545 <212> TYPE: DNA

546 <213> ORGANISM: Artificial sequence

W--> 547

547 <223> OTHER INFORMATION: polylinker

548 <400> SEQUENCE: 17

549 cgcggccgcg ctagcgtcga c

21

551 <210> SEQ ID NO: 18

552 <211> LENGTH: 7

553 <212> TYPE: DNA

554 <213> ORGANISM: Artificial sequence

W--> 555

555 <223> OTHER INFORMATION: Shine-Dalgarno Sequence

E--> 556 <400> SEQUENCE: 18

557 aggaggu

7

E--> 558 ??

E--> 560 ??

E--> 562 ??

E--> 564 ??

E--> 571 1/14

pls delete

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L:6 M:283 W: Missing Blank Line separator, <120> field identifier
 L:7 M:283 W: Missing Blank Line separator, <130> field identifier
 L:8 M:270 C: Current Application Number differs, Replaced Current Application No
 L:8 M:271 C: Current Filing Date differs, Replaced Current Filing Date
 L:8 M:283 W: Missing Blank Line separator, <160> field identifier
 L:9 M:283 W: Missing Blank Line separator, <210> field identifier
 L:13 M:283 W: Missing Blank Line separator, <220> field identifier
 L:13 M:256 W: Invalid Numeric Header Field, <220> has non-blank data
 L:15 M:283 W: Missing Blank Line separator, <400> field identifier
 L:15 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:1,Line#:14
 L:43 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:1
 L:66 M:283 W: Missing Blank Line separator, <220> field identifier
 L:66 M:256 W: Invalid Numeric Header Field, <220> has non-blank data
 L:68 M:283 W: Missing Blank Line separator, <400> field identifier
 L:68 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:2,Line#:67
 L:91 M:283 W: Missing Blank Line separator, <220> field identifier
 L:91 M:256 W: Invalid Numeric Header Field, <220> has non-blank data
 L:93 M:283 W: Missing Blank Line separator, <400> field identifier
 L:93 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:3,Line#:92
 L:140 M:283 W: Missing Blank Line separator, <220> field identifier
 L:140 M:256 W: Invalid Numeric Header Field, <220> has non-blank data
 L:142 M:283 W: Missing Blank Line separator, <400> field identifier
 L:142 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:4,Line#:141
 L:164 M:283 W: Missing Blank Line separator, <220> field identifier
 L:164 M:256 W: Invalid Numeric Header Field, <220> has non-blank data
 L:165 M:259 W: Allowed number of lines exceeded, <220> FEATURE:
 L:167 M:283 W: Missing Blank Line separator, <400> field identifier
 L:167 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:5,Line#:166
 L:219 M:283 W: Missing Blank Line separator, <220> field identifier
 L:219 M:256 W: Invalid Numeric Header Field, <220> has non-blank data
 L:220 M:259 W: Allowed number of lines exceeded, <220> FEATURE:
 L:221 M:283 W: Missing Blank Line separator, <400> field identifier
 L:250 M:200 E: Mandatory Header Field missing, <220> Tag not found for SEQ ID#:7
 L:250 M:283 W: Missing Blank Line separator, <400> field identifier
 L:259 M:200 E: Mandatory Header Field missing, <220> Tag not found for SEQ ID#:8
 L:259 M:283 W: Missing Blank Line separator, <400> field identifier
 L:268 M:200 E: Mandatory Header Field missing, <220> Tag not found for SEQ ID#:9
 L:268 M:283 W: Missing Blank Line separator, <400> field identifier
 L:287 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:10
 L:288 M:200 E: Mandatory Header Field missing, <220> Tag not found for SEQ ID#:10
 L:288 M:283 W: Missing Blank Line separator, <400> field identifier
 L:370 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:11
 L:371 M:200 E: Mandatory Header Field missing, <220> Tag not found for SEQ ID#:11
 L:371 M:283 W: Missing Blank Line separator, <400> field identifier
 L:378 M:200 E: Mandatory Header Field missing, <220> Tag not found for SEQ ID#:12
 L:378 M:283 W: Missing Blank Line separator, <400> field identifier
 L:387 M:200 E: Mandatory Header Field missing, <220> Tag not found for SEQ ID#:13
 L:387 M:283 W: Missing Blank Line separator, <400> field identifier

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L:399 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:14
L:400 M:200 E: Mandatory Header Field missing, <220> Tag not found for SEQ ID#:14
L:400 M:283 W: Missing Blank Line separator, <400> field identifier
L:459 M:254 E: No. of Bases conflict, LENGTH:Input:3504 Counted:3540 SEQ:14
L:500 M:200 E: Mandatory Header Field missing, <220> Tag not found for SEQ ID#:15
L:500 M:283 W: Missing Blank Line separator, <400> field identifier
L:530 M:200 E: Mandatory Header Field missing, <220> Tag not found for SEQ ID#:16
L:530 M:283 W: Missing Blank Line separator, <400> field identifier
L:547 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:17
L:548 M:200 E: Mandatory Header Field missing, <220> Tag not found for SEQ ID#:17
L:548 M:283 W: Missing Blank Line separator, <400> field identifier
L:555 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:18
L:556 M:200 E: Mandatory Header Field missing, <220> Tag not found for SEQ ID#:18
L:556 M:283 W: Missing Blank Line separator, <400> field identifier
L:558 M:334 E: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:1
L:560 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:18
L:560 M:334 E: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:1
L:562 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:18
L:562 M:334 E: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:1
L:564 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:18
L:564 M:334 E: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:1
L:571 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:18
L:571 M:254 E: No. of Bases conflict, LENGTH:Input:14 Counted:8 SEQ:18
L:571 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:2
L:571 M:252 E: No. of Seq. differs, <211> LENGTH:Input:7 Found:8 SEQ:18